



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/088,594
Source: PCT10
Date Processed by STIC: 3/28/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
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U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
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Revised 01/29/2002



Does Not Comply PCT10
Corrected Diskette Needed

Errors on pp. 2 + 7

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/088,594

DATE: 03/28/2002
TIME: 10:30:26

Input Set : A:\EP.txt
Output Set: N:\CRF3\03282002\J088594.raw

3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
5 <120> TITLE OF INVENTION: Novel Transaldolase
7 <130> FILE REFERENCE: 11236WO1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/088,594
C--> 10 <141> CURRENT FILING DATE: 2002-03-21
12 <150> PRIOR APPLICATION NUMBER: JP 99/266548
13 <151> PRIOR FILING DATE: 1999-09-21
15 <160> NUMBER OF SEQ ID NOS: 3
17 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

19 <210> SEQ ID NO: 1 *length should be 1080!*
 20 <211> LENGTH: 360 *A coding sequence is always a nucleic sequence.*
 21 <212> TYPE: PRT *Thus, response can only be DNA or RNA.*
 22 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
 24 <400> SEQUENCE: 1
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 27 Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu
 28 1 5 10 15
 30 gac gac ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt 96
 31 Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val
 32 20 25 30
 34 att gag gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc 144
 35 Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe
 36 35 40 45
 38 gca gca gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag 192
 39 Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
 40 50 55 60
 42 ctc aag gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc 240
 43 Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
 44 65 70 75 80
 46 atc gac gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag 288
 47 Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
 48 85 90 95
 50 tcc tcc aac ggc tac gac ggc cgc gtg tcc atc gag gtt gac cca cgt 336
 51 Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
 52 100 105 110
 54 atc tct gct gac cgc gac gca acc ctg gct cag gcc aag gag ctg tgg 384
 55 Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
 56 115 120 125
 58 gca aag gtt gat cgt cca aac gtc atg atc aag atc cct gca acc cca 432

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62	ggt	tct	ttg	cca	gca	atc	acc	acc	gac	gct	ttg	gct	gag	ggc	atc	agc	gtt	480
63	Gly	Ser	Leu	Pro	Ala	Ile	Thr	Asp	Ala	Leu	Ala	Glu	Gly	Ile	Ser	Val		
64	145					150					155				160			
66	aac	gtc	acc	ttg	atc	ttc	tcc	gtt	gct	cgc	tac	cgc	gag	gtc	atc	gct		528
67	Asn	Val	Thr	Leu	Ile	Phe	Ser	Val	Ala	Arg	Tyr	Arg	Glu	Val	Ile	Ala		
68						165				170			175					
70	gcg	tac	atc	gag	gga	atc	aag	cag	gca	gct	gca	aac	ggc	cac	gac	gta		576
71	Ala	Tyr	Ile	Glu	Gly	Ile	Lys	Gln	Ala	Ala	Ala	Asn	Gly	His	Asp	Val		
72						180			185			190						
74	tcc	aag	atc	cac	tct	gtg	gct	tcc	ttc	gtc	tcc	cgc	gtc	gac	gtt		624	
75	Ser	Lys	Ile	His	Ser	Val	Ala	Ser	Phe	Phe	Val	Ser	Arg	Val	Asp	Val		
76						195			200			205						
78	gag	atc	gac	aag	cgc	ctc	gag	gca	atc	gga	tcc	gat	gag	gct	ttg	gct		672
79	Glu	Ile	Asp	Lys	Arg	Leu	Glu	Ala	Ile	Gly	Ser	Asp	Glu	Ala	Leu	Ala		
80						210			215			220						
82	ctg	cgc	ggc	aag	gca	ggc	gtt	gcc	aac	gct	cag	cgc	gct	tac	gtc	gtg		720
83	Leu	Arg	Gly	Lys	Ala	Gly	Val	Ala	Asn	Ala	Gln	Arg	Ala	Tyr	Ala	Val		
84						225			230			235			240			
86	tac	aag	gag	ctt	ttc	gac	gcc	gag	ctg	cct	gaa	ggt	gcc	aac	act		768	
87	Tyr	Lys	Glu	Leu	Phe	Asp	Ala	Ala	Glu	Leu	Pro	Glu	Gly	Ala	Asn	Thr		
88						245			250			255						
90	cag	cgc	cca	ctg	tgg	gca	tcc	acc	ggc	gtg	aag	aac	cct	gcg	tac	gct		816
91	Gln	Arg	Pro	Leu	Trp	Ala	Ser	Thr	Gly	Val	Lys	Asn	Pro	Ala	Tyr	Ala		
92						260			265			270						
94	gca	act	ctt	tac	gtt	tcc	gag	ctg	gct	ggt	cca	aac	acc	gtc	aac	acc		864
95	Ala	Thr	Leu	Tyr	Val	Ser	Glu	Leu	Ala	Gly	Pro	Asn	Thr	Val	Asn	Thr		
96						275			280			285						
98	atg	cca	gaa	ggc	acc	atc	gac	gct	gtt	ctg	gaa	ctg	ggc	aac	ctg	cac		912
99	Met	Pro	Glu	Gly	Thr	Ile	Asp	Ala	Val	Glu	Leu	Gly	Asn	Leu	His			
100						290			295			300						
102	ggg	gac	acc	ctg	tcc	aaa	tcc	ggc	gca	gaa	gct	gac	gct	gtg	ttc	tcc		960
103	Gly	Asp	Thr	Leu	Ser	Asn	Ser	Ala	Ala	Glu	Ala	Asp	Ala	Val	Phe	Ser		
104						305			310			315			320			
106	cag	ctt	gag	gct	ctg	ggc	gtt	gac	ttg	gca	gat	gtc	ttc	cag	gtc	ctg		1008
107	Gln	Leu	Glu	Ala	Leu	Gly	Val	Asp	Leu	Ala	Asp	Val	Phe	Gln	Val	Leu		
108						325			330			335						
110	gag	acc	gag	ggt	gtg	gac	aag	ttt	gtt	gct	tct	tgg	agc	gaa	ctg	ctt		1056
111	Glu	Thr	Glu	Gly	Val	Asp	Lys	Phe	Val	Ala	Ser	Trp	Ser	Glu	Leu	Leu		
112						340			345			350						
E-->	114	gag	tcc	atg	gaa	gct	cgc	ctg	aag							1080	!	
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163	<211>	LENGTH:	4108															
164	<212>	TYPE:	DNA															
165	<213>	ORGANISM:	Corynebacterium	glutamicum	ATCC31388													
167	<221>	NAME/KEY:	CDS															

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168 <222> LOCATION: (373)..(2472)
 170 <221> NAME/KEY: CDS
 171 <222> LOCATION: (2643)..(3722)
 173 <400> SEQUENCE: 3
 174 tcgagagttt gaagggtcc gattcgttcc gttcgtgacg ctttgtgagg ttttttgacg 60
 176 ttgcaccgtt ttgcttgcgg aacattttc ttttccttc gggttttcga gaattttcac 120
 178 ctacaaaagc ccacgtcaca gtcggcagac ttaagattgg tcacacccctt gacacatttg 180
 180 aaccacagtggttataaaa tgggttcaac atcactatgg ttagaggtgt tgacgggtca 240
 182 gattaagcaa agactactt cggggtagat cacccttgcc aaatttgaat caattaacct 300
 184 aagtctgatcatac ggtatctaacc aaaacgaacc aaaacttgg tcccggttta 360
 186 acccaggaag ga atg acc acc ttg acg ctg tca cct gaa ctt cag gcg ctc 411
 187 Met Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu
 188 1 5 10
 190 act gta cgc aat tac ccc tct gat tgg tcc gat gtg gac acc aag gct 459
 191 Thr Val Arg Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala
 192 15 20 25
 194 gta gac act gtt cgt gtc ctc gct gca gac gct gta gaa aac tgt ggc 507
 195 Val Asp Thr Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly
 196 30 35 40 45
 198 tcc ggc cac cca ggc acc gca atg agc ctg gct ccc ctt gca tac acc 555
 199 Ser Gly His Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr
 200 50 55 60
 202 ttg tac cag cgg gtt atg aac gta gat cca cag gac acc aac tgg gca 603
 203 Leu Tyr Gln Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala
 204 65 70 75
 206 ggc cgt gac cgc ttc gtt ctt tct tgt ggc cac tcc tct ttg acc cag 651
 207 Gly Arg Asp Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln
 208 80 85 90
 210 tac atc cag ctt tac ttg ggt gga ttc ggc ctt gag atg gat gac ctg 699
 211 Tyr Ile Gln Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu
 212 95 100 105
 214 aag gct ctg cgc acc tgg gat tcc ttg acc cca gga cac cct gag tac 747
 215 Lys Ala Leu Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr
 216 110 115 120 125
 218 cgc cac acc aag ggc gtt gag atc acc act ggc cct ctt ggc cag ggt 795
 219 Arg His Thr Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly
 220 130 135 140
 222 ctt gca tct gca gtt ggt atg gcc atg gct gct cgt cgt gag cgt ggc 843
 223 Leu Ala Ser Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly
 224 145 150 155
 226 cta ttc gac cca acc gct gct gag ggc gaa tcc cca ttc gac cac cac 891
 227 Leu Phe Asp Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His
 228 160 165 170
 230 atc tac gtc att gct tct gat ggt gac ctg cag gaa ggt gtc acc tct 939
 231 Ile Tyr Val Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser
 232 175 180 185
 234 gag gca tcc tcc atc gct ggc acc cag cag ctg ggc aac ctc atc gtc 987
 235 Glu Ala Ser Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val
 236 190 195 200 205

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238	tcc	tgg	gat	gac	aac	cgc	atc	tcc	atc	gaa	gac	aac	act	gag	atc	gct	1035
239	Phe	Trp	Asp	Asp	Asn	Arg	Ile	Ser	Ile	Glu	Asp	Asn	Thr	Glu	Ile	Ala	
240					210				215						220		
242	tcc	aaa	gag	gac	gtt	gtt	gct	cgt	tac	aag	gct	tac	ggc	tgg	cag	acc	1083
243	Phe	Asn	Glu	Asp	Val	Val	Ala	Arg	Tyr	Lys	Ala	Tyr	Gly	Trp	Gln	Thr	
244					225				230						235		
246	att	gag	gtt	gag	gct	ggc	gag	gac	gtt	gca	gca	atc	gaa	gtc	gca	gtg	1131
247	Ile	Glu	Val	Glu	Ala	Gly	Glu	Asp	Val	Ala	Ala	Ile	Glu	Ala	Ala	Val	
248					240				245						250		
250	gct	gag	gct	aag	aag	gac	acc	aag	cga	cct	acc	ttc	atc	cgc	gtt	cgc	1179
251	Ala	Glu	Ala	Lys	Lys	Asp	Thr	Lys	Arg	Pro	Thr	Phe	Ile	Arg	Val	Arg	
252					255				260						265		
254	acc	atc	atc	ggc	tcc	cca	gct	cca	acc	atg	atg	aac	acc	ggt	gct	gtg	1227
255	Thr	Ile	Ile	Gly	Phe	Pro	Ala	Pro	Thr	Met	Met	Asn	Thr	Gly	Ala	Val	
256					270				275						280		285
258	cac	ggt	gct	gct	ctt	ggc	gca	gct	gag	gtt	gca	gca	acc	aag	act	gag	1275
259	His	Gly	Ala	Ala	Leu	Gly	Ala	Ala	Glu	Val	Ala	Ala	Thr	Lys	Thr	Glu	
260					290				295						300		
262	ctt	gga	ttc	gat	cct	gag	gct	cac	tcc	ggc	atc	gac	gat	gag	gtt	atc	1323
263	Leu	Gly	Phe	Asp	Pro	Glu	Ala	His	Phe	Ala	Ile	Asp	Asp	Glu	Val	Ile	
264					305				310						315		
266	gct	cac	acc	cgc	tcc	ctc	gca	gag	cgc	gct	gca	cag	aag	aag	gct	gca	1371
267	Ala	His	Thr	Arg	Ser	Leu	Ala	Glu	Arg	Ala	Ala	Gln	Lys	Lys	Ala	Ala	
268					320				325						330		
270	tgg	cag	gtc	aag	ttc	gat	gag	tgg	gca	gct	gcc	aac	cct	gag	aac	aag	1419
271	Trp	Gln	Val	Lys	Phe	Asp	Glu	Trp	Ala	Ala	Ala	Asn	Pro	Glu	Asn	Lys	
272					335				340						345		
274	gct	ctg	tcc	gat	cgc	ctg	aat	tcc	cgt	gag	ctt	cca	ggc	ggc	tac	gct	1467
275	Ala	Leu	Phe	Asp	Arg	Leu	Asn	Ser	Arg	Glu	Leu	Pro	Ala	Gly	Tyr	Ala	
276					350				355						360		365
278	gac	gag	ctc	cca	aca	tgg	gat	gca	gat	gag	aag	ggc	gtc	gca	act	cgt	1515
279	Asp	Glu	Leu	Pro	Thr	Trp	Asp	Ala	Asp	Glu	Lys	Gly	Val	Ala	Thr	Arg	
280					370				375						380		
282	aag	gct	tcc	gag	gct	gca	ctt	cag	gca	ctg	ggc	aag	acc	ctt	cct	gag	1563
283	Lys	Ala	Ser	Glu	Ala	Ala	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Leu	Pro	Glu	
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286	ctg	tgg	ggc	ggt	tcc	gct	gac	ctc	gca	ggt	tcc	aat	acc	acc	gtg	atc	1611
287	Leu	Trp	Gly	Gly	Ser	Ala	Asp	Leu	Ala	Gly	Ser	Asn	Asn	Thr	Val	Ile	
288					400				405						410		
290	aag	ggc	tcc	cct	tcc	ttc	ggc	cct	gag	tcc	atc	tcc	acc	gag	acc	tgg	1659
291	Lys	Gly	Ser	Pro	Ser	Phe	Gly	Pro	Glu	Ser	Ile	Ser	Thr	Glu	Thr	Trp	
292					415				420						425		
294	tct	gct	gag	cct	tac	ggc	cgt	aat	ctg	cac	ttc	ggt	atc	cgt	gag	cac	1707
295	Ser	Ala	Glu	Pro	Tyr	Gly	Arg	Asn	Leu	His	Phe	Gly	Ile	Arg	Glu	His	
296					430				435						440		445
298	gct	atg	gga	tcc	atc	ctc	aac	ggc	att	tcc	ctc	cac	ggt	ggc	acc	cgc	1755
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300					450				455						460		
302	cca	tac	ggt	gga	acc	tcc	ctc	atc	tcc	tcc	gac	tac	atg	cgt	cct	gca	1803

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307	Val	Arg	Leu	Ala	Ala	Leu	Met	Glu	Thr	Asp	Ala	Tyr	Tyr	Val	Trp	Thr	
308						480			485				490				
310	cac	gac	tcc	atc	ggt	ctg	ggc	gaa	gat	ggc	cca	acc	cac	cag	cct	gtt	
311	His	Asp	Ser	Ile	Gly	Leu	Gly	Glu	Asp	Gly	Pro	Thr	His	Gln	Pro	Val	
312						495			500				505				
314	gaa	acc	ttg	gct	gcg	ctg	cgc	gcc	atc	cca	ggt	ctg	tcc	gtc	ctg	cgt	
315	Glu	Thr	Leu	Ala	Ala	Leu	Arg	Ala	Ile	Pro	Gly	Leu	Ser	Val	Leu	Arg	
316	510					515				520				525			
318	cct	gca	gat	gcg	aat	gag	acc	gcc	cag	gct	tgg	gct	gca	gca	ctt	gag	
319	Pro	Ala	Asp	Ala	Asn	Glu	Thr	Ala	Gln	Ala	Trp	Ala	Ala	Ala	Leu	Glu	
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332						575			580				585				
334	atg	ggc	tcc	ggc	tcc	gag	ggc	gtt	cag	ctt	gca	gtt	aac	gct	gcg	aaa	gct
335	Met	Gly	Ser	Gly	Ser	Glu	Val	Gln	Leu	Ala	Val	Asn	Ala	Ala	Lys	Ala	
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339	Leu	Glu	Ala	Glu	Gly	Val	Ala	Ala	Arg	Val	Val	Ser	Val	Pro	Cys	Met	
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342	gat	tgg	tgc	cag	gag	cag	gac	gca	gag	tac	atc	gag	tcc	gtt	ctg	cct	
343	Asp	Trp	Phe	Gln	Glu	Gln	Asp	Ala	Glu	Tyr	Ile	Glu	Ser	Val	Leu	Pro	
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347	Ala	Ala	Val	Thr	Ala	Arg	Val	Ser	Val	Glu	Ala	Gly	Ile	Ala	Met	Pro	
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355	Phe	Gly	Ala	Ser	Ala	Asp	Tyr	Gln	Thr	Leu	Phe	Glu	Lys	Phe	Gly	Ile	
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367																Met Ser	

1

W--> 368

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Input Set : A:\EP.txt
Output Set: N:\CRF3\03282002\J088594.raw

369	cac att gat gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac	2696
370	His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp	
W--> 371	5 10 15	
373	ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt att gag	2744
374	Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu	
W--> 375	20 25 30	
377	gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc gca gca	2792
378	Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala	
W--> 379	35 40 45 50	
381	gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag ctc aag	2840
382	Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys	
W--> 383	55 60 65	
385	gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc atc gac	2888
386	Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp	
W--> 387	70 75 80	
389	gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc	2936
390	Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser	
W--> 391	85 90 95	
393	aac ggc tac gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct	2984
394	Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser	
W--> 395	100 105 110	
397	gct gac cgc gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag	3032
398	Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys	
W--> 399	115 120 125 130	
401	gtt gat cgt cca aac gtc atg atc aag atc cct gca acc cca ggt tct	3080
402	Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser	
W--> 403	135 140 145	
405	ttg cca gca atc acc gac gct ttg gct gag ggc atc agc gtt aac gtc	3128
406	Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val	
W--> 407	150 155 160	
409	acc ttg atc ttc tcc gtt gct cgc tac cgc gag gtc atc gct gcg tac	3176
410	Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Tyr	
W--> 411	165 170 175	
413	atc gag gga atc aag cag gca gct gca aac ggc cac gac gta tcc aag	3224
414	Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val Ser Lys	
W--> 415	180 185 190	
417	atc cac tct gtg gct tcc ttc gtc tcc cgc gtc gac gtt gag atc	3272
418	Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile	
W--> 419	195 200 205 210	
421	gac aag cgc ctc gag gca atc gga tcc gat gag gct ttg gct ctg cgc	3320
422	Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Leu Arg	
W--> 423	215 220 225	
425	ggc aag gca ggc gtt gcc aac gct cag cgc gct tac gct gtg tac aag	3368
426	Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val Tyr Lys	
W--> 427	230 235 240	
429	gag ctt ttc gac gcc gcc gag ctg cct gaa ggt gcc aac act cag cgc	3416
430	Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg	
W--> 431	245 250 255	
433	cca ctg tgg gca tcc acc ggc gtg aag aac cct gcg tac gct gca act	3464

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/088,594

DATE: 03/28/2002
TIME: 10:30:26

Input Set : A:\EP.txt
Output Set: N:\CRF3\03282002\J088594.raw

434	Pro	Leu	Trp	Ala	Ser	Thr	Gly	Val	Lys	Asn	Pro	Ala	Tyr	Ala	Ala	Thr	
W--> 435	260			265			270										
437	ctt	tac	gtt	tcc	gag	ctg	gct	ggt	cca	aac	acc	gtc	aac	acc	atg	cca	3512
438	Leu	Tyr	Val	Ser	Glu	Leu	Ala	Gly	Pro	Asn	Thr	Val	Asn	Thr	Met	Pro	
W--> 439	275			280			285									290	
441	gaa	ggc	acc	atc	gac	gct	gtt	ctg	gaa	ctg	ggc	aac	ctg	cac	ggt	gac	3560
442	Glu	Gly	Thr	Ile	Asp	Ala	Val	Leu	Glu	Leu	Gly	Asn	Leu	His	Gly	Asp	
W--> 443	295			300			305										
445	acc	ctg	tcc	aac	tcc	gcg	gca	gaa	gct	gac	gct	gtg	ttc	tcc	cag	ctt	3608
446	Thr	Leu	Ser	Asn	Ser	Ala	Ala	Glu	Ala	Asp	Ala	Val	Phe	Ser	Gln	Leu	
W--> 447	310			315			320										
449	gag	gct	ctg	ggc	gtt	gac	ttg	gca	gat	gtc	ttc	cag	gtc	ctg	gag	acc	3656
450	Glu	Ala	Leu	Gly	Val	Asp	Leu	Ala	Asp	Val	Phe	Gln	Val	Leu	Glu	Thr	
W--> 451	325			330			335										
453	gag	ggt	gtg	gac	aag	ttt	gtt	gct	tct	tgg	agc	gaa	ctg	ctt	gag	tcc	3704
454	Glu	Gly	Val	Asp	Lys	Phe	Val	Ala	Ser	Trp	Ser	Glu	Leu	Leu	Glu	Ser	
W--> 455	340			345			350										
457	atg	gaa	gct	cgc	ctg	aag	tagaatcagc	acgctgcata	agtaaacggcg								3752
458	Met	Glu	Ala	Arg	Leu	Lys											
W--> 459	355			360													
461	acatgaaatc	gaatttagttc	gatcttatgt	ggccgttaca	catcttcat	taaaagaaaagg											3812
463	atcgtgacgc	taccatcgta	agcacaaaca	cgacccccctc	cagctggaca	aaccactgc											3872
465	gcgacccgca	ggataaaacga	ctcccccgca	tgcgtggccc	ttccggcatg	gtgatcttcg											3932
467	gtgtcaactgg	cgacttggct	cgaaggaagc	tgctccccgc	catttatgat	ctagcaaacc											3992
469	gcggattgct	gcccccagga	ttctcggtgg	tagttacgg	ccgcccgcga	tggccaaag											4052
471	aagactttga	aaaatacgtc	cgcgtatgcgc	caagtgtgg	tgctcgta	gaattc											4108

E--> 476 10/12 -delete

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/088,594

DATE: 03/28/2002
TIME: 10:30:27

Input Set : A:\EP.txt
Output Set: N:\CRF3\03282002\J088594.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:114 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:115 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=1
L:116 M:252 E: No. of Seq. differs, <211>LENGTH:Input:360 Found:368 SEQ:1
L:368 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:391 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:395 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:419 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:423 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:427 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:431 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:443 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:451 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:455 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:476 M:254 E: No. of Bases conflict, LENGTH:Input:12 Counted:4109 SEQ:3
L:476 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:476 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4108 Found:4109 SEQ:3